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**PERSPECTIVES ON SPONGE-CYANO-BACTERIAL SYMBIOSES.** Memoirs of the Queensland Museum 44: 154. 1999:- Insights on the evolution of sponge-cyanobacterial symbioses are drawn from biogeographic and molecular data. The taxonomic and geographic distribution of sponge-cyanobacteria associations is analysed after surveying their occurrence at eight localities in the Eastern and Western Tropical Pacific, and the Carihbean. Three methods - fluorescent microscopy, thin layer chromatography and transmission electron microscopy - were used to infer the existence of endosymbiotic cyanobacteria.

Thirty-eight species, representing 17 families and 11 orders of Demospongiae, and one family and order of Calcarea, are added to the list of sponges involved in these associations. This number represents an increase of more than 50% over previously known occurrences of this type of metazoan-microbial association. However this increase of species numbers represents only an addition of twelve genera and two families to the taxonomic distribution of these associations. Species from 26 of the 72 recognised Demospongiae families, and 3 of the 17 recognised Calcarea families are found to harbour cyanobacterial endosymbionts. These data suggest a rather restricted taxonomic range for sponge-cyanobacterial assemblages, and invites a search for evolutionary trends among the families involved. The genera with highest number of species harbouring cyanobacteria are: Aplysina (10 spp.), Xestospongia (7 spp.), Dysidea (5 spp.), and Theonella (5 spp.). Although the updated list of spongecyanobacterial assemblages shows a few biogeographic trends, the understanding of the evolution of these associations requires the study of more extensive geographic areas.

The use of 16S rDNA analysis to understand the phylogenetic relationships of endosymbiotic eyanobacteria is discussed. Genetic analyses promise to shed light on the understanding of the evolution and specificity of these associations. 16S rDNA gene analyses carried out so far suggest that sponge-eyanobacterial assemblages comprise diverse and complex evolutionary histories, some of which might share evolutionary pathways with other important marine symbiotic assemblages involving cyanobacteria.  $\Box$  Porifera, cyanobacteria endosymbioses, biogeography, evolutionary trends, 16S ribosomal genes.

M.C. Diaz (email: diaz(acats.ucsc.edu), Institute of Marine Sciences, A316 EMS, University of California Santa Cruz, CA 95064, USA; B.B. Ward, Institute of Marine Sciences and Ocean Sciences Department, A316 EMS, University of California Santa Cruz, CA 95064, USA: 1 June 1998.